

The Founder Mutation *MSH2**1906G→C Is an Important Cause of Hereditary Nonpolyposis Colorectal Cancer in the Ashkenazi Jewish Population

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Hereditary nonpolyposis colorectal cancer (HNPCC) is caused by mutations in the mismatch-repair genes. We report here the identification and characterization of a founder mutation in *MSH2* in the Ashkenazi Jewish population. We identified a nucleotide substitution, *MSH2**1906G→C, which results in a substitution of proline for alanine at codon 636 in the *MSH2* protein. This allele was identified in 15 unrelated Ashkenazi Jewish families with HNPCC, most of which meet the Amsterdam criteria. Genotype analysis of 18 polymorphic loci within and flanking *MSH2* suggested a single origin for the mutation. All colorectal cancers tested showed microsatellite instability and absence of *MSH2* protein, by immunohistochemical analysis. In an analysis of a population-based incident series of 686 Ashkenazi Jews from Israel who have colorectal cancer, we identified 3 (0.44%) mutation carriers. Persons with a family history of colorectal or endometrial cancer were more likely to carry the mutation than were those without such a family history ($P = .042$), and those with colorectal cancer who carried the mutation were, on average, younger than affected individuals who did not carry it ($P = .033$). The mutation was not detected in either 566 unaffected Ashkenazi Jews from Israel or 1,022 control individuals from New York. In hospital-based series, the 1906C allele was identified in 5/463 Ashkenazi Jews with colorectal cancer, in 2/197 with endometrial cancer, and in 0/83 with ovarian cancer. When families identified by family history and in case series are included, 25 apparently unrelated Ashkenazi Jewish families have been found to harbor this mutation. Although this pathogenic mutation is not frequent in the Ashkenazi Jewish population (accounting for 2%–3% of colorectal cancer in those whose age at diagnosis is <60 years), it is highly penetrant and accounts for approximately one-third of HNPCC in Ashkenazi Jewish families that fulfill the Amsterdam criteria.

Introduction

Hereditary nonpolyposis colorectal cancer (HNPCC) (MIM 114500) is the most common hereditary colorec-

tal cancer syndrome, accounting for ~2% of incident cases (Aaltonen et al. 1998; Peltomaki 2001). When established family history criteria, known as “the Amsterdam criteria” (Vasen et al. 1991, 1999), are used to ascertain families as affected with HNPCC, disease-causing mutations in the mismatch-repair genes *MLH1* (MIM 120436) and *MSH2* (MIM 120435) are identified in 50%–80% of the families (Peltomaki 2001). In certain populations, founder mutations explain a substantial fraction of HNPCC. For example, in Finland, two mutations in *MLH1* (a 3.5-kb genomic deletion affecting

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Table 1

Clinicopathological Characteristics of Affected Carriers of the *MSH2**1906G→C Mutation Who Were Initially Identified at Participating Clinical Centers

Family	Center ^a	Sex	Clinical Feature(s) (Age [years] at Diagnosis of Cancer) ^b	HNPCC Criteria ^c	MSI Status ^d	Immunohistochemistry for MSH2 ^e
1	MU	F	Endometrial carcinoma (44), CRC (62)	AC I	MSI-H	NA
	MU	M	CRC (35)	AC I	MSI-H	NA
2	UW	M	TCC-RP (33), metastatic adenocarcinoma to liver PSU (43)	Father, B 2 and 3	NA	MSH2 absent (liver)
	MSKCC	M	TCC-U (42), TCC-B (45), cecal carcinoma (47), T cell non-Hodgkin lymphoma (68)	B 2 and 3	MSI-H	NA
3	UW	M	Cecal carcinoma (40), second CRC (52)	AC I	NA	NA
	MSKCC	F	CRC (30)	AC I	MSI-H	MSH2 absent
4	MSKCC	M	Colonic tubulo-villous adenoma with CIS (45)	AC I	MSI-H	MSH2 absent
5	IGR	M	CRC (37 and 61), TCC-U (71), leg sarcoma (72), TCC-B (75), GBM (78)	B 2 and 3	NA	NA
	IGR	F	Sigmoid carcinoma (47), transverse-colon carcinoma (48)	B 2 and 3	MSI-H	MSH2 absent
6	CHCC	F	CRC (46)	AC I	MSI-H	Focally, weakly present
7	JHU	M	CRC (37)	AC I	MSI-H	MSH2 absent
8	MSKCC	F	CRC (48)	AC I	MSI-H	NA
	MSKCC	M	Rectal carcinoma (28)	AC I	NA	NA
9	MSKCC	F	Ovarian carcinoma (41)	None ^f	MSI-H ^g	NA
10	OSU	F	Endometrial carcinoma (36), sigmoid carcinoma (53), recurrent recto-sigmoid carcinoma (55)	AC I	MSI-H	MSH2 absent
11	UH	M	CRC (31), second CRC (34)	B 2	MSI-H	MSH2 absent
12	UH	F	Endometrial carcinoma (?)	NA	MSI-H	MSH2 absent
13	OSU	M	CRC × 3 (43, 63, and 70)	B 2	MSI-H	MSH2 absent
14	RMH	M	TCC-U (53), CRC (55)	AC I	MSI-H ^h	NA
15	RMH	F	Sigmoid carcinoma (42), endometrial and ovarian carcinoma (54)	AC I	MSI-H ⁱ	MSH2 absent

NOTE.—Results for probands of families 16–25 are not shown because these cases were not ascertained as part of the clinic-based series; for details, see text.

^a MU = McGill University (Montreal); UW = University of Washington (Seattle); IGR = Institut Gustave Roussy (Paris); CHCC = City of Hope Cancer Center (Duarte, CA); JHU = Johns Hopkins University (Baltimore); OSU = Ohio State University (Columbus); UH = University of Heidelberg (Heidelberg, Germany); RMH = Royal Melbourne Hospital (Melbourne).

^b CRC = colorectal cancer; TCC-RP = transitional cell carcinoma-renal pelvis; PSU = primary site unknown; TCC-U = transitional cell carcinoma-ureter; TCC-B = transitional cell carcinoma-bladder; CIS = carcinoma in situ; GBM = glioblastoma multiforme.

^c AC = Amsterdam Criteria; B = Bethesda Guidelines; NA = not available.

^d MSI-H = microsatellite instability high; NA = not available. MSI was performed on CRCs, unless otherwise stated.

^e Performed on CRCs, unless otherwise stated.

^f No criteria were fulfilled, but see figure 1.

^g MSI was performed on the ovarian cancer.

^h MSI was performed on the CRC.

ⁱ MSI was performed on the endometrial cancer.

Table 2**Clinical and laboratory Data on Ashkenazi Jewish Families That Meet Amsterdam Criteria 1 or 2**

INDIVIDUAL	KINDRED	MSI	1906 C ALLELE	OTHER MISMATCH- REPAIR MUTATIONS	No. OF	
					CRCs	Other HNPCC- Related Cancers
1	175	Present	Present	None detected	5	1
2	284	Present	Absent	Not tested	4	0
3	1580	Present	Present	Not detected	3	4
4	1614	Absent ^a	Absent	None detected	3	1
5	1692	Present	Present	Not tested	5	0
6	1915	Absent	Absent	Not tested	3	0
7	2101	Absent	Absent	Not tested	3	0
8	2650	Present	Present	Absent	3	3
9	3051	Not tested	Absent	<i>MLH1</i> *1411del4	3	1
10	3274	Present	Absent	<i>MSH6</i> *3987insGTCA	3	0
11	3571	Not tested	Absent	Not tested	6	0
12	3762	Not tested	Absent	Not tested	7	0

NOTE.—All families were ascertained at MSKCC during 1995–2001.

^a The tissue tested for MSI in these families consisted of adenomatous polyps: in kindred 1614, a polyp was tested in the proband, and analysis of *MLH1* and *MSH2* was performed; in kindred 3762, one adenomatous polyp was tested. MSI-H was not detected.

exon 16, known as “mutation 1,” and a splice-acceptor site mutation of exon 6, known as “mutation 2”) account for 63% of all disease-causing mutations identified in families with HNPCC (Nystrom-Lahti et al. 1995; Moio et al. 1996). Mutations 1 and 2 have been calculated to have originated 16–43 and 5–21 generations ago, respectively. A Swiss group identified an *MLH1* mutation (*MLH1**2141G→A, resulting in the substitution W714X, in several apparently unrelated families from the Valais region of Switzerland. Haplotype analysis indicates that this is a founder mutation, although the age of the mutation could not be precisely determined (Hutter et al. 1996). Another possible founder mutation, an 1.8-kb deletion involving exon 11 of *MLH1*, resulting in an mRNA transcript with a deletion of exons 10–11, has been reported in China (Chan et al. 2001). Recent haplotype studies of the recurrent *MSH2* mutation (*MSH2**IVS5+3A→T), which disrupts the 3' splice site of exon 5, leading to the deletion of this exon from the *MSH2* mRNA, confirm that the mutation has multiple origins but is a founder mutation in Newfoundland, Canada (Desai et al. 2000). To our knowledge, no other founder mutations in *MSH2* have been reported. The identification of founder mutations not only is of research interest but has practical implications, in that ethnic-specific mutation analysis can be offered before a more general search for disease-associated mutations is attempted. This approach has been particularly successful when genetic testing for *BRCA1/2* is offered to the Ashkenazi Jewish population, in which three founder mutations account for the majority of all *BRCA1/2* mutations (Shiri-Sverdlov et al. 2000).

We previously have identified the mutation *MSH2**1906G→C, which causes a substitution of pro-

line for alanine at amino acid residue 636 (A636P) (Yuan et al. 1999). Here, we describe the genetic characterization of this mutation. We also conducted mutation-frequency studies in unselected series of Ashkenazi Jewish individuals with colorectal, endometrial, breast, or ovarian cancer, ascertained in North America and Israel, as well as in an ongoing, large population-based case-control study in northern Israel. We have also estimated the magnitude of the contribution of this mutation to HNPCC in the Ashkenazi Jewish population.

Subjects, Material, and Methods

Nonsystematic Series of Mutation Carriers

The *MSH2**1906G→C mutation was first identified in an Ashkenazi Jewish woman from a typical family with HNPCC (Yuan et al. 1999). The family fulfilled the Amsterdam criteria, as described elsewhere (Vasen et al. 1991). At approximately the same time, the mutation was independently identified in North America, Europe, and Australia, in unrelated individuals, and it was first posted on the Web site of the International Collaborative Group on Hereditary Non-Polyposis Colorectal Cancer (see the “Choose a Mutation Database” Web page), by Bressac de Paillerets and colleagues, in 1998. Analysis of the mutant protein in a yeast-based assay indicated that the mutation compromises *MSH2* function (Yuan et al. 1999). In the following 3 years, probands from several other North American, European, Israeli, and Australian kindreds with an excess of colorectal or other HNPCC-related cancers were found to carry this mutation (table 1). These probands and

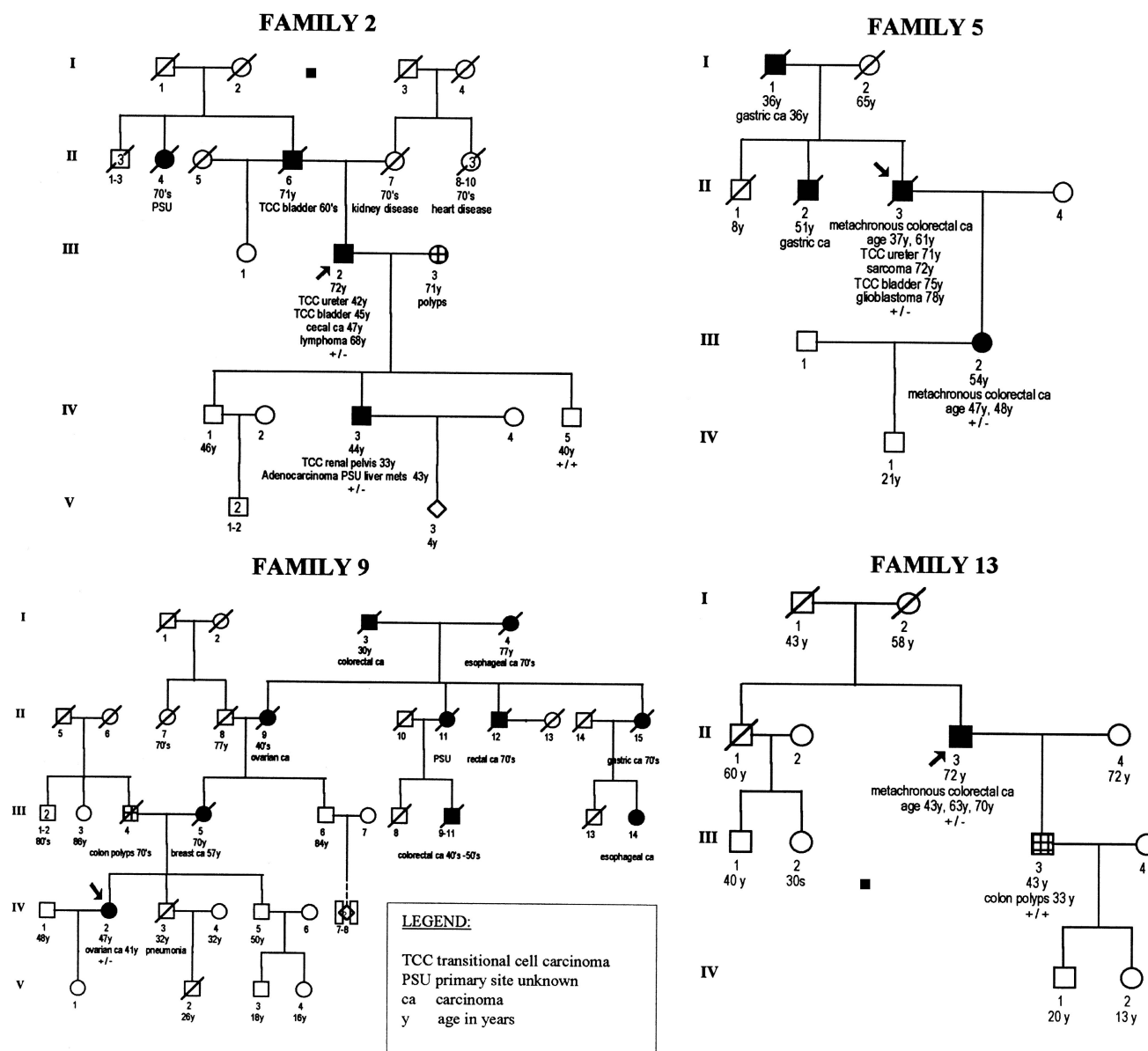


Figure 1 Representative families with the *MSH2**1906G→C mutation. Carriers of *MSH2**1906G→C are indicated by "+/-"; tested non-carriers are indicated by "+/+"; all other individuals are untested. Notably, none of these families fulfil the Amsterdam criteria but, nevertheless, a priori are very likely to carry germline mutations in mismatch-repair genes.

other family members were studied further. All these individuals were seen in cancer-genetics clinics in various settings in the nine centers that contributed case subjects to this study. All clinic and population studies were conducted under the auspices of protocols approved by Institutional Review Boards.

Having identified the *MSH2**1906G→C mutation in these selected families, we wished to establish more firmly its disease-causing nature and to determine its frequency in (a) families with a high probability of carrying a germline mutation in a mismatch-repair gene, (b) unselected individuals with HNPCC-related cancers

(colorectal, ovary, and endometrial), (c) a population-based series of individuals with colorectal cancer and age- and sex-matched control individuals, (d) women with breast cancer who had a family history of colorectal or ovarian cancer, and (e) unaffected North American control individuals. By studying all of these groups, we sought to determine, in a comprehensive fashion, the contribution that this mutation makes to HNPCC-related cancers in the Jewish population and to establish, at least in part, the phenotypic range of expression of this mutation.

Because of the different types of ascertainment criteria,

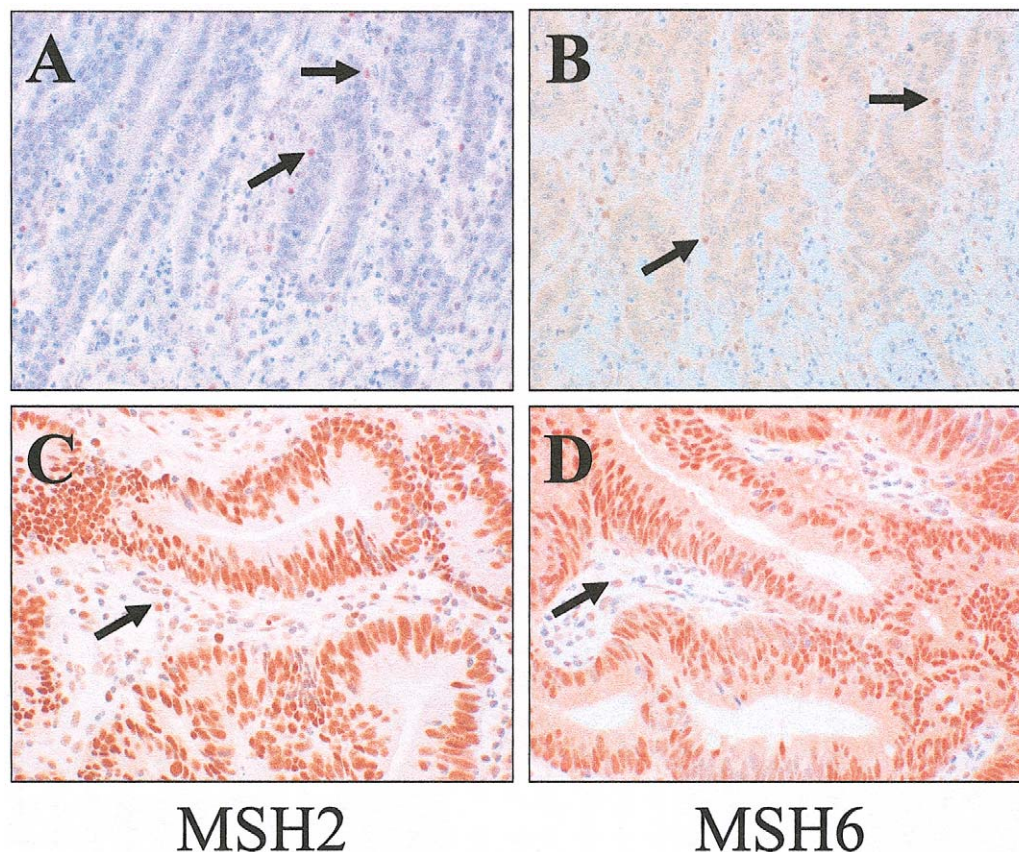


Figure 2 Immunohistochemical staining of MSH2 (A) and MSH6 (B), in the woman in family 3 who has colorectal cancer and carries the *MSH2**1906G→C mutation (tables 1 and 2) and in control samples from colorectal tumors in which MSH2 (C) and MSH6 (D) are expressed. The colonic adenocarcinoma is moderately differentiated, with relatively well-formed glands infiltrating the stromal tissue. Positive immunoreactivity with antibodies to MSH2 and MSH6 is represented by the presence of brown staining in the nuclei. There is a complete absence of nuclear staining of both MSH2 and MSH6 in the tumor cells, whereas a few scattered small lymphocytes show brown labeling in their nuclei (arrow). The presence of nuclear staining in lymphocytes serves as an internal positive control. The stain for MSH6 shows some cytoplasmic labeling both in the tumor cells and in some stromal cells. The significance of such cytoplasmic staining in this patient is unclear but is likely a reflection of nonspecific background staining.

we made efforts to ensure that none of the families included in the different series were identical or closely related. These efforts included checking last names and examining pedigrees. Except for the Memorial Sloan-Kettering Cancer Center (MSKCC) series (discussed below), none of the persons who carried the *MSH2**1906G→C mutation whose identities were known to us are closely related. Carriers identified in anonymized series may or may not be related to persons in the patient-identified series.

Hospital-Based Series

Families with colorectal cancer.—At MSKCC, 109 kindreds were ascertained during 1995–2001. Probandes were systematically ascertained either by a family-history questionnaire administered to persons visiting the gastrointestinal endoscopy and oncology clinics, by personal interview of persons undergoing surgery for co-

lorectal cancer, or by referrals to the Clinical Genetics service. To the extent possible, the relevant cancer diagnoses identified by the proband were confirmed by obtaining pathology reports or death certificates. Of the 109 families ascertained, 37 were Ashkenazi Jewish; 12 of these 37 families fulfilled the Amsterdam criteria for HNPCC, whereas the other 25 families were HNPCC-like, defined as containing three or more cases of colorectal cancer occurring at any age in first- or second-degree relatives. In 6 of the 109 families in which there were either two or more individuals with adenomatous polyps or at least one individual with colorectal cancer diagnosed before age 50 years, the presence of an adenomatous polyp was counted as a surrogate for a colorectal cancer. At least one affected individual from each of these 37 families was tested for the *MSH2**1906G→C mutation. Five of these 37 families were also ascertained in the case-series part of the study, but they were not

Table 3**MSH2*1906C Data: Frequency, Family History of Cancer, and Age at Diagnosis, in the MECC Study**

A. Consecutive Colorectal Cancer Cases				
	NO. OF CASES/NO. OF CONTROL INDIVIDUALS			
	Ashkenazi Jews	Sephardic Jews	OTHER ^a	TOTAL
1906C	3/0	0/0	0/0	3
WT sequence	<u>683/566</u>	<u>159/185</u>	<u>76/78</u>	<u>1,747</u>
Total	686/566	159/185	76/78	1,750
B. Family History of Colorectal or Endometrial Cancer in a First-Degree Relative, in Ashkenazi Jews with Colorectal Cancer ^b				
	Positive Family History	Negative Family History	Total ^c	
1906C	2	1	3	
WT sequence	<u>79</u>	<u>571</u>	<u>650</u>	
Total	81	572	653	
C. Age at Diagnosis in Ashkenazi Jews with Colorectal Cancer				
	Age at Diagnosis <60 years	Age at Diagnosis ≥60 years	Total ^d	
1906C	2	1	3	
WT sequence	<u>77</u>	<u>606</u>	<u>683</u>	
Total	79	607	686	

^a Arab (107), Bedouin (1), Druze (18), and “non-Arab/non-Jew” (28).

^b Family history was not available for 33 cases.

^c $P = .042$ (by Fisher’s exact test, two sided).

^d $P = .036$ (by Fisher’s exact test, two sided).

counted twice in the total number of identified families (see previous section and results below). In addition, 25 individuals from the 37 families (1 individual per family—10 from HNPCC and 15 from “HNPCC-like” families) were tested for microsatellite instability (Boland et al. 1998).

Consecutive cases of patients with colorectal cancer.—Two series were studied. The first series comprised 108 Ashkenazi Jewish patients with incident colorectal cancer who were treated at MSKCC. The DNA samples were anonymized after sex, age, and ethnicity had been recorded, and, therefore, personal identifiers and family-history information are not available for these 108 individuals. A total of 41 women and 67 men were tested. The mean age at diagnosis was 61.0 ± 11.7 years. The second series comprised 564 patients with histopathologically proven colorectal cancer who were diagnosed and treated at Elias Sourasky Medical Center in Tel Aviv, during January 1998–December 2001, and who were eligible for participation. Clinical data regarding family history of cancer, age at diagnosis, and relevant tumor-

associated data were obtained from a personal questionnaire, review of pathological reports, and data from medical records. Of these 564 patients, 355 were Ashkenazi Jews and 209 were non-Ashkenazi Jews. All were screened for the presence of the *MSH2**1906G→C mutation, and, therefore, in the two hospital series, 463 Ashkenazi Jewish individuals with colorectal cancer were tested for this mutation.

Historical cohort of incident HNPCC-related cancers.—DNA extracted from paraffin-embedded tumors from two historical cohorts of Ashkenazi Jewish patients, one with ovarian carcinoma ($n = 83$) and the other with endometrial cancer ($n = 197$), ascertained at MSKCC were resequenced for the *MSH2**1906G→C mutation. The clinicopathological characteristics of the cancers in these two cohorts have been described elsewhere (Boyd et al. 2000; Levine et al. 2001). Women known to be carrying an Ashkenazi Jewish founder mutation in either *BRCA1* or *BRCA2* were not included in this study.

Familial breast cancer.—Two hundred seventy-one Ashkenazi Jewish breast cancer probands who had a family history of colorectal cancer or ovarian cancer were collected from various centers in the United States during the course of studies of breast cancer genetics. In the present study, these samples were analyzed for the *MSH2**1906G→C mutation, at the Division of Medical Genetics, University of Washington, Seattle. The criteria for inclusion in this study were as follows: (a) wild type (WT) for the three founder Ashkenazi Jewish *BRCA1/2* mutations, genotyped by sequencing (no other *BRCA1/2* genotyping was performed) and (b) at least one case of ovarian or colorectal cancer occurring at any age in first-degree relatives.

Population-Based Studies

The Molecular Epidemiology of Colorectal Cancer (MECC) study is a population-based case-control study of colorectal cancer in northern Israel. Residents of the northern and Haifa districts of Israel who are diagnosed with histopathologically confirmed, incident colorectal cancer between March 31, 1998, and December 31, 2002, are eligible as cases. Population-based control individuals are identified from the Clalit Health Services database and are individually matched to cases by exact year of birth, gender, and clinic. Interim data for 921 cases and 829 control individuals from this ongoing case-control study were available for the present analysis. All were screened for the *MSH2**1906G→C mutation. Of the 921 cases, 686 were Ashkenazi Jews; of the 829 control individuals, 566 were Ashkenazi Jews.

The New York Cancer Project (NYCP) is an ongoing cohort study with current ascertainment of >18,000 volunteers (ages 30–69 years) who live in the New York

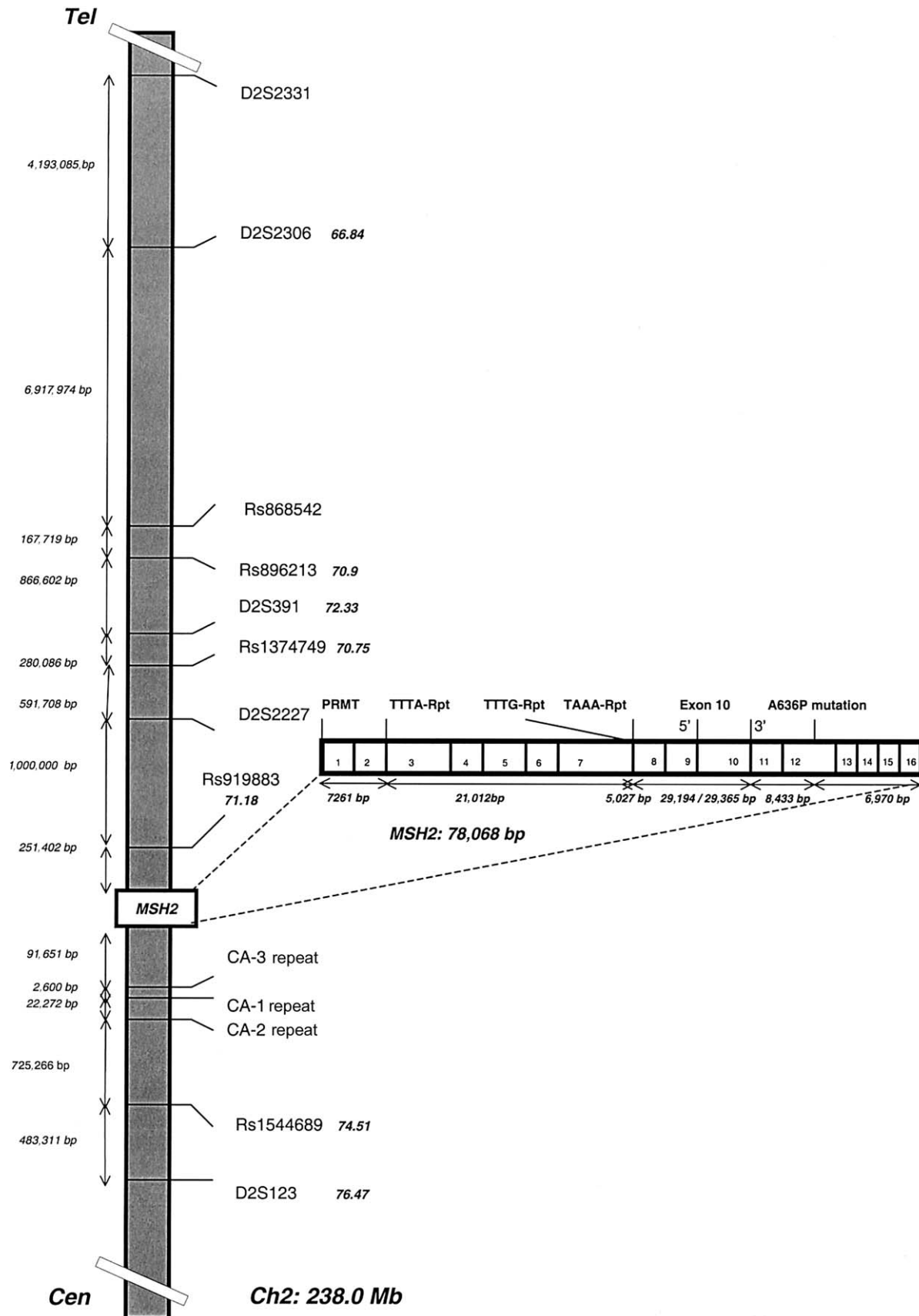
Table 4

Genotypes and Haplotypes for Carriers of the *MSH2*1906G→C* Mutation

MARKER	GENOTYPE OR HAPLOTYPE ^a													
	Family 1		Family 2		Family 3		Family 4		Family 5		Family 6		Family 7	
	MON702	II: 11	UWc	SK-M138b	S-M112	S-M112	487	3G393-	CH0346-	JHU SG	Allele A	Allele B	SKM1387	B307
D2S2331	4/4	3,4	7,4	4,4	3,3	2/3	4	2	4	7,3	2,7	4,4	4,4	3/4
D2S2306	2,4	4,4	4,4	1,4	1,4	4/4	3	4	3	3,4	4,4	1,4	2,4	3/4
Rs868542	C,T	T,T	C,C	—	C,C	—	—	—	—	C,C	T,T	C,C	C,T	C/T
Rs896213	A/A	A,A	G,A	G,A	A,A	G/A	A	A	A	A,A	G,A	A,A	G,A	G/A
D2S391	3,2	4,2	2,2	4,3	1,2	2/2	1	2	2	4,2	4,2	4,2	1,2	2/2
Rs1374749	A/A	G,A	G,A	—	A,A	—	A	A	A	A,A	A,A	G,A	G,A	G/A
D2S2227	2,3	2,3	2,3	2,3	2,3	2/3	2	3	3	3,3	1,3	2,3	2,3	3/3
Rs919883	A/G	A,G	G,G	A,G	A,G	—	G	G	G	A,G	G,G	G,G	G,G	G/G
TTTA repeat	292/288	284,288	288,288	288,288	296,288	296/288	284	288	288	292,288	292,288	288,288	288,288	296/288
TTTG repeat	255/255	255,255	259,255	259,255	255,255	255/255	259	255	255	255,255	255,255	259,255	255,255	255/255
TAAA repeat	177/177	185,177	181,177	177,177	177,177	177/177	193	177	177	177,177	177,177	185,177	177,177	177/177
5' Exon 10	A/A	A,A	A,A	A,A	A,A	A/A	A	A	A	A,A	A,A	A,A	A,A	A/A
3' Exon 10	G/G	A,G	G,G	G,G	G,G	G/G	A	G	G	G,G	G,G	G,G	G,G	G/G
A636P mutation	G/C	G,C	G,C	G,C	G,C	G/C	G	C	C	G,C	G,C	G,C	G,C	G/C
CA-3 repeat	141/141	139,139	141,139	141,139	141,139	135/139	141	139	139	139,139	141,139	141,139	141,139	137/139
CA-1 repeat	147/149	147,143	145,143	147,143	145,143	147/143	147	143	143	147,143	145,143	131,143	147,143	147/143
CA-2 repeat	254/250	246,250	254,250	250,250	250,250	250/250	254	250	250	254,250	250,250	250,250	250,250	254/250
Rs1544689	C/T	C,T	T,T	T,T	T,T	T/C	C	C	C	T,T	T,T	T,C	T,T	C/T
D2S123	6/6	1,4	4,6	4,6	6,6	4/6	5	6	6	2,4	2,6	4,6	2,6	4/6

NOTE.—No DNA was available from family 10 (see table 1); families 16–19 are not shown in table 1; they were ascertained as part of the hospital-based studies.

^a Boldface italics denote a linked allele; a slash (/) denotes phase; a comma (,) denotes no phase.



Metropolitan area. Subjects were enrolled at seven hospitals and six community centers in New York City, and they provided consent for genetics studies on deidentified DNA samples prepared from blood. We obtained samples from a subset of persons who are healthy, unaffected by cancer, and self-identified as Jewish. At the time of acquisition of the DNA specimens, there were 2,172 Jews enrolled in the NYCP; in the present study, we used DNA samples from 1,022 of these individuals.

Pathological Evaluation and Immunohistochemical and Microsatellite-Instability Analyses

Pathological evaluation and immunohistochemistry.—Centralized pathology review was not performed, but each cancer in individuals subjected to mutation analysis was verified at the referring center. When tissue was available, immunohistochemistry was performed, with modifications of a protocol described elsewhere (Marcus et al. 1999).

Microsatellite instability.—Assays were performed on microdissected DNA from paraffin-embedded blocks, by use of a consensus panel of markers, as described elsewhere (Boland et al. 1998). Radiolabeled PCR products amplified by use of the “Bethesda panel” of markers were scored for the appearance of novel locus-specific bands in the tumor but not in the DNA of normal tissue. A tumor was scored as MSI-H when the proportion of successfully typed loci exhibiting novel bands was $\geq .3$; a tumor was scored as non-MSI-H when the proportion was $< .3$.

Molecular Analyses

*Characterization of the *MSH2**1906G→C mutation.*—The *MSH2**1906G→C mutation was originally identified in the clinical and research laboratories of participating institutions, by several different methods. All available DNA samples were resequenced in the Molecular Diagnostics Laboratory at Sir M. B. Davis-Jewish General Hospital, by the Visible Genetics OpenGene system (Visible Genetics). The primer pairs used for se-

quencing the PCR-amplified exon 12 of *MSH2* are shown in the “Methods for Detection of the *MSH2**1906G→C Mutation” section and table A1, both in the Appendix, in the online version of this article. For the sequencing procedure, reagents from Visible Genetics were used. In brief, an aliquot of the PCR product (3–8 μ l, depending on the yield) was mixed with sequencing buffer, dimethyl sulfoxide, Cy5.5 M13 primer, water, and Thermosequenase enzyme (Amersham), according to instructions included as an insert to the kit. This mixture was then distributed (5 μ l/tube) into four tubes (labeled “A,” “C,” “G,” and “T”) containing 3 μ l of the termination mix. The mixture was then cycled for 35 cycles, on a thermal cycler, as follows: 94°C for 30 s, 55°C for 30 s, and 70°C for 45 s. The thermal cycling was initiated with a 2-min denaturation step at 94°C and was terminated with a 5-min extension step at 70°C. At the end, 6.0 μ l of the loading dye (containing formamide) was added to each of the four tubes, to stop the sequencing reaction. The sequencing samples were then denatured at 80°C for 3 min and then immediately were placed on ice. Two microliters was then loaded onto a 6% acrylamide gel containing 6 M urea. Data acquisition and base calling were achieved by use of Gene Objects software (Visible Genetics).

Denaturing high-performance liquid chromatography (DHPLC) was also used to identify mutations in DNA prepared from blood. A complete description of the methods used is provided in the “Methods for Detection of the *MSH2**1906G→C Mutation” section in the Appendix, in the online version of this article.

For the unselected series of endometrial and ovarian cancers, for which the source of DNA was archival pathological tissue, direct sequencing was used to detect the mutations, as described above. For the University of Washington series of breast cancer cases, screening for the *MSH2**1906G→C mutation was performed by SSCP using sense primer 5'-CCAATGCAGACACTCAATGATGTG-3' and antisense primer 5'-CCACAAAGCCCCAA-AAACCAGG-3'. An allele-specific oligohybridization

Figure 3 Schematic representation of *MSH2* and surrounding regions of chromosome 2. Marker loci and genetic distances are shown. This map is based on information provided by The Genome Database and the National Center for Biotechnology Information (see the “Single Nucleotide Polymorphism” Web page). We used the “BLAST Search Genome” Web page (August 2001 freeze) of the University of California, Santa Cruz, to obtain the relative genetic positions of these markers. The relative positions of some markers have been published elsewhere (Green et al. 1994; Desai et al. 2000), but some of that positional information was erroneous. Single-nucleotide polymorphisms (SNPs) were identified by use of “The SNP Consortium Ltd.” Web site. The *MSH2* map was designed in accordance with data provided by the ICG-HNPCC. Intragenic markers have been described elsewhere (Desai et al. 2000). Alongside the vertical portion of the ideogram, we have indicated the positions of markers, according to the recombination map presented by Kong et al. (2002). Note that the positions of D2S391 and Rs1374749 with respect to surrounding markers are uncertain. According to data available at the Golden Path Web site (see the “UCSC Genome Informatics” Web page), Rs1374749 is centromeric of D2S391, whereas according to the recombination map presented by Kong et al. it is telomeric; Kong et al.’s recombination map also places Rs919883 telomeric of D2S391. There are discrepancies between the recombination map and the physical map presented by Kong et al. If the true map order is tel-D2S391-Rs137479-Rs896213-Rs919883-cen (based primarily on physical data), then all markers from *MSH2* up to and including Rs137479 are completely conserved, whereas D2S391 and markers beyond it are not. At this time, it is not possible to synthesize all of the available mapping data into one consistent marker order. For further details, see the Electronic-Database Information and Results sections.

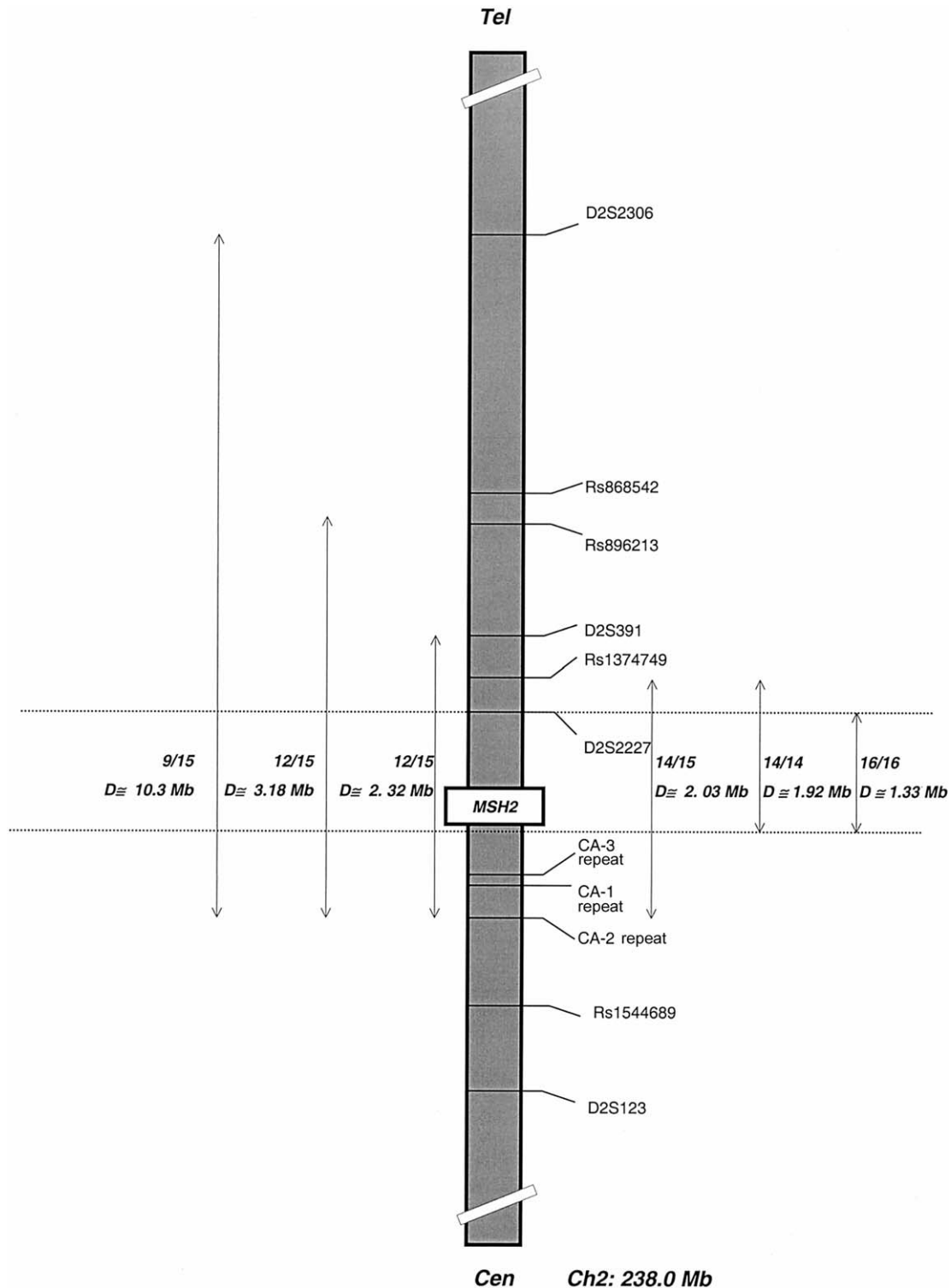


Figure 4 Schematic map of chromosome 2, showing extent of potential haplotype sharing. Sixteen unrelated families were studied. The position of *MSH2* is indicated, and the positions of markers are as shown in figure 3. “D” denotes distance (in Mb). The double-headed vertical arrows indicate the extent of the possible haplotype sharing in different groups of mutation carriers, and the ends of the arrows indicate the last marker that is conserved in the indicated fraction of probands studied; for example, probands from 9 of 15 families share a haplotype that could extend over a maximum of ~10.3 Mb. The proportion of families sharing the same haplotype increases from left to right. For details, see the text.

Table 5**Frequency of *MSH2**1906G→C in Ashkenazi Jewish Individuals with Cancer**

STUDY GROUP OR HOSPITAL	SITE OF CANCER	ASCERTAINMENT SCHEME	NO. OF CASES	
			1906C/Total (%)	1906C Diagnosed at Age <60 years/ Total 1906C (%)
Mount Sinai Hospital, Toronto	Colorectum	Incident cases, hospital based	0/196 ^a	0/23 ^b
MSKCC	Colorectum	Incident cases, hospital based	1/108 (.92)	1/42 (2.39)
Northern and Haifa Districts, Israel	Colorectum	Incident cases, population based	3/686 (.44)	2/75 (2.67)
Elias Sourasky Medical Center, Tel Aviv	Colorectum	Incident cases, hospital based	4/355 (1.1)	NA
MSKCC	Ovary	Incident cases, hospital based	0/83	0/22
MSKCC	Endometrium	Incident cases, hospital based	2/197 (1.02)	0/55
University of Washington, Seattle	Breast	Part of nationwide BRCA1/2-related studies	0/271	NA

^a Source: Yuan et al. (1999).^b Source: Dr. M. Redston (personal communication).

assay was optimized to screen for *MSH2**1906G→C mutations among cases and control individuals in the large population-based series. A complete description of the methods is provided in the “Methods for Detection of the *MSH2**1906G→C Mutation” section and table A1, both in the Appendix, in the online version of this article.

Haplotype analysis.—Haplotype analysis was performed on each individual by use of single-nucleotide polymorphisms (SNPs) and microsatellites on chromosome 2. The tetranucleotide repeat (TTTA, TTG, or TAAA) and dinucleotide repeat (CA-1, CA-2, or CA-3) microsatellites were visualized by fragment-size analysis by the OpenGene System. The PCR products for these markers were diluted fivefold with sterile water. We added 5 μ l of loading buffer to 1 μ l of the diluted PCR product and denatured the mixture at 80°C for 3 min and then loaded 2 μ l onto a 6% polyacrylamide gel. The other microsatellite markers—D2S2331, D2S391, D2S2306, D2S123, and D2S2227—were amplified by PCR using [³⁵S]-dATP. PCR products were separated on denaturing acrylamide gels and were visualized by autoradiography. The SNPs Rs896213 and Rs1544689 were analyzed by sequencing using a Cy5.5 DEAZA dye sequencing kit (Visible Genetics) and the OpenGene System; the other SNPs—Rs919883, Rs868542, and Rs1374749—were amplified by PCR, and the products were digested by restriction enzymes *Sfa*NI, *Bsm*I, and *Pml*I (New England Biolabs), respectively, according to the manufacturer’s instructions. Primer sequences and PCR conditions are shown in the “Methods for Detection of the *MSH2**1906G→C Mutation” section and table A1, both in the Appendix, in the online version of this article.

Somatic-Cell Hybridization

Epstein-Barr virus-transformed cells were available from an individual in family 7 (table 1). Somatic-cell

hybrids containing a maternally or paternally derived chromosome 2 were obtained from GMP Genetics.

Statistical Analyses

Association analyses.—Odds ratios were calculated by use of 2 × 2 tables, and Gart’s method was used for the 95% CI (Fleiss 1981). *P* values reported are the results of two-tailed Fisher’s exact tests, because some of the cells had expected counts of <5. The frequency of the *MSH2**1906G→C mutation in different subgroups was estimated by the sign test, and exact 95% CIs were calculated for the proportions by the Clopper-Pearson method. Statistical analyses were performed by SAS version 8.00 (SAS Institute).

Frequency of haplotypes in the Ashkenazi Jewish population.—Because the number of Ashkenazi Jewish families available was not large, haplotypes were reconstructed by the program PHASE (Stephens et al. 2001), which uses Bayesian methods to predict the haplotype distribution, conditional on observed genotypes. The algorithm is implemented by Gibbs sampling, which is a type of Markov chain–Monte Carlo algorithm (Gilks et al. 1996). For nine markers (*PRMT* to *CA-2* [Desai et al. 2000]; see the “Methods for Detection of the *MSH2**1906G→C Mutation” section and table A1, both in the Appendix, in the online version of this article), we used DNA from 54 Ashkenazi Jews from Israel (obtained from the National Laboratory for the Genetics of Israeli Populations, Tel Aviv University) to construct the haplotypes. We seeded the program with 12 known haplotypes. We used both the 11 unlinked haplotypes that were established by analysis of the individuals carrying the *MSH2**1906G→C mutation and the haplotype associated with the mutation itself. Ten simulations were run from different starting points, and the results were used to estimate the frequency of the linked haplotype in the Ashkenazi Jewish population.

Results

*MSH2*1906G→C Occurs in Ashkenazi Jews with Colorectal and Other Cancers*

In addition to the first reported kindred, a total of 24 individuals from 14 unrelated families were initially identified, at various centers in North America, Europe, and Australia, as being carriers of the *MSH2**1906G→C mutation. These cases were not identified during the course of specific mutation-prevalence studies but were seen in clinical cancer-genetics clinics. Subsequently, it became apparent that, of these 15 originally ascertained families, 5 (families 2–4, 8, and 9; table 1) were also represented in the systematic series of families with HNPCC ascertained at MSKCC (families 175, 1580, 1692, and 2650 are listed in table 2, and families 1431 and 2475 are listed in table A2, in the Appendix in the online version of this article). We have included these five families in the analysis of families with HNPCC but have not counted them twice in the final totals. In 12 of these 15 families, the probands identified themselves and their parents as Ashkenazi Jewish; in 2 families, ethnic origins could not be ascertained; in 1 family, the family's last name and country of origin suggest Jewish origins. The clinicopathological features of the cancers and the family histories of the probands (including the initial proband from MON702) are shown in table 1. Particularly noteworthy is the wide range of cancers seen in carriers of the *MSH2**1906G→C mutation. Although the Amsterdam criteria were not met in all families, the cancer histories in all the families were suggestive of mismatch-repair–gene mutations. For example, family 2 did not fulfil these criteria because cancer was said to arise in the bladder (rather than in the ureter) in the paternal grandfather of the proband. In fact, this family is the first reported kindred with a *MSH2* mutation and with three generations of individuals diagnosed with transitional cell carcinoma of the urothelium. In family 5, the proband was diagnosed with six separate cancers: metachronous colorectal cancer, metachronous urothelial transitional cell carcinoma, a soft-tissue sarcoma, and finally, at the age of 78 years, a glioblastoma multiforme (fig. 1). One individual in family 14 was diagnosed with seven cancers (colorectal cancer on three separate occasions, ureteric cancer twice, and stomach and bladder cancer). The proband in this family also had a ureteric cancer (table 1).

*MSH2*1906G→C Is Associated with Microsatellite Instability, Absence of MSH2 Protein, and an Alteration in MSH2 Crystal Structure*

When tumor tissue was available, testing for microsatellite instability was performed. All 15 colorectal cancers tested (as well as 1 ovarian cancer and 1 endometrial

cancer) exhibited an MSI-H phenotype (table 1). In all 10 tumors examined by immunohistochemistry, MSH2 protein (table 1 and fig. 2) was highly reduced or absent. When MSH6 was also assessed (fig. 2), this protein was also missing. This latter finding is not unexpected, because together MSH2 and MSH6 form a complex. The crystal structure of MutS has recently been determined in *Thermophilus aquaticus* (TAQ), by Obmolova et al. (2000), and in *Escherichia coli*, by Lamers et al. (2000). Position 636 is only two codons from the highly conserved amino acid motif (i.e., RH) that appears to be important for interdomain interactions. The alanine itself is not conserved either in yeast MSH2, MSH3, MSH4, MSH5, or MSH6 or in human MSH3 or MSH6. Nevertheless, in TAQ, the equivalent codon, 555, is for alanine. Altering the crystal structure of TAQ *in silico*, we showed that the homologous mutation A555P interferes with the carbonyl group of neighboring phenylalanine. This change probably affects ATP binding or protein/protein interactions (W. Yang, personal communication). Taken together, these findings suggest strongly that the *MSH2**1906G→C mutation is disease causing.

*MSH2*1906G→C Is an Important Cause of HNPCC in the Ashkenazi Jewish Population*

We wished to estimate what proportion of autosomal dominant familial colorectal cancer could be caused by this mutation. To do this, we screened 37 affected individuals from MSKCC who met either the HNPCC criteria ($n = 12$) or the HNPCC-like criteria ($n = 25$); of the 37 individuals tested, 6 (mutation prevalence .16; 95% CI .06–.32) carried the *MSH2**1906G→C mutation. In the 12 families that met the Amsterdam criteria (table 2), the mutation prevalence was .33 (95% CI .10–.65). The mutation was found in one of the families meeting the HNPCC-like but not the Amsterdam criteria (see the “Analysis of the *MSH2**1906G→C Mutation in New York Families with Colorectal Cancer” section and table A2, both in the Appendix, in the online version of this article). Of the 12 families with Amsterdam criteria–fulfilling HNPCC, 6 carried a mutation in either *MSH2* or *MLH1*; consequently, the four *MSH2**1906G→C mutations accounted for .67 (95% CI .22–.96) of all identified mutations in Ashkenazi Jewish families with HNPCC that fulfill the Amsterdam criteria.

*Frequency of the MSH2*1906C Allele in Population-Based Cases and Control Individuals*

To determine the frequency of the 1906C allele in an unselected series of Jewish individuals with or without colorectal cancer, we genotyped 1,750 Israeli individuals (including 686 Ashkenazi Jewish cases and 566 Ash-

kenazi Jewish control individuals) ascertained in the ongoing MECC study. The ethnic breakdown and results are shown in table 3. Among 686 Ashkenazi Jewish colorectal cancer cases, we identified 3 carriers of the 1906C allele; no carriers were identified among 566 Ashkenazi Jewish control individuals. Thus, in this large unselected series, 0.44% (95% CI 0.09%–1.27%) of colorectal cancers occurring in Ashkenazi Jewish individuals is attributable to the 1906C allele. The allele was not in statistically significant excess in Ashkenazi Jews with colorectal cancer compared with Ashkenazi Jewish control individuals ($P = .26$) (table 3A). To further estimate the population frequency of this mutation, we tested 1,022 Jewish individuals enrolled in the NYCP. No carriers were detected; thus, 0/1,588 Ashkenazi Jewish people carry this allele (the upper limit for the 95% CI is 0.23%).

Dichotomizing the study group on the basis of either positive family history (table 3B) or age at diagnosis (table 3C) reveals the influence that the mutation has on the presentation of colorectal cancer in carriers of the 1906C allele. The absence of this mutation in non-Ashkenazi Jewish individuals with colorectal cancer and/or a family history consistent with HNPCC (table 3A) does not prove that this mutation is absent from other populations, but it does appear that the mutation is likely to be very rare in non-Ashkenazi Jewish populations.

*Frequency of the MSH2*1906C Allele in Hospital-Based Consecutive Series of Cases of Colorectal Cancer*

A series of 564 individuals with colorectal cancer who were diagnosed in Tel Aviv were screened for the presence of the *MSH2**1906G→C mutation; of these 564, 355 (63%) were Ashkenazi Jews and 209 were of non-Ashkenazi Jewish origins. Four mutation carriers were detected, all of Ashkenazi Jewish origin, whose ancestors lived in either Poland ($n = 2$) or Russia ($n = 2$). Thus, in this hospital series, 1.1% (95% CI 0.31%–2.9%) of Israeli Ashkenazi Jews with colorectal cancer carry the *MSH2**1906G→C mutation. Two of the four cases were diagnosed at age <60 years. Two of the four affected carriers also had previous colonic polyps, and, of three individuals who had details of their family history, two reported first-degree relatives with colorectal cancer. The frequency of the 1906C allele was also estimated in 108 incident cases of colorectal cancer in Ashkenazi Jews who had surgery at MSKCC. We identified one carrier in this series, an affected man diagnosed with colorectal cancer at age 28 years. This mutation carrier was one of only five individuals in this series who were diagnosed at age <40 years, compared with no carriers identified in the remaining 103 tested ($P = .046$). This finding further supports the contention that the

*MSH2**1906G→C mutation causes early-onset colorectal cancer and is a rare allele in the Ashkenazi Jewish population.

*Frequency of the MSH2*1906C Allele in Unselected Series of Women with HNPCC-Related Cancers*

To characterize the contribution that the *MSH2**1906G→C mutation makes to adenocarcinoma of the endometrium, ovary, and breast, we studied three series of women. Two of these series were from MSKCC—one series comprised 197 Ashkenazi Jewish women diagnosed with endometrial adenocarcinoma from December 1986 to August 1998, and the other series comprised 83 Ashkenazi Jewish women diagnosed with ovarian cancer at the same institution during the same period. Two (1.02%; 95% CI 0.1%–3.6%) women with endometrial adenocarcinoma (diagnosed at ages 72 and 76 years) were found to carry the *MSH2**1906G→C mutation, whereas none of the 83 women with ovarian cancer (mean age at diagnosis, 64.6 years; SD 11.8 years) carried this mutation (95% CI 0%–4.3%). The ages at diagnosis of endometrial adenocarcinoma are older than the mean age for this series (66.3 years; SD 11.1 years). A third series consisted of 271 U.S. Ashkenazi Jewish breast cancer probands who had a family history of either colorectal cancer or ovarian cancer and who had been collected from various centers in the United States. No mutations were identified in these women (95% CI 0%–1.4%).

Haplotype Analysis

To determine the haplotype associated with the chromosome bearing the *MSH2**1906G→C mutation in one individual (from family 7) (tables 1 and 4), somatic-cell hybrids carrying only the mutation-bearing human chromosome 2 were analyzed at polymorphic loci spanning an ~16-Mb region that flanks *MSH2* (fig. 3). An 18-marker haplotype was constructed. This haplotype consisted of 7 SNPs and 11 polymorphic microsatellite loci (see the “Methods for Detection of the *MSH2**1906G→C Mutation” section and table A1, both in the Appendix, in the online version of this article). Using human-genome sequence data recently made available at the “Golden Path” Web site of the University of California, Santa Cruz (see the “UCSC Genome Informatics” Web page), we mapped previously reported markers CA-1, CA-2, and CA-3 (Desai et al. 2000) as being situated 3' of *MSH2*. Figure 3 illustrates the physical distances, in base pairs, between each marker, as well as these markers' relationship to *MSH2*. On the basis of the Golden Path Web site's map order of August 2001 (see the “UCSC Genome Informatics” Web page), the most likely order of the loci that we tested is tel-D2S2331–D2S2306–Rs868542–Rs896213–D2S391–Rs1374749–D2S2227–Rs919883–

[5'MSH2-TTTA repeat-TTTG repeat-TAAA repeat-E105'-E103'-1906C/3'MSH2]-CA-3 repeat-CA-1 repeat-CA-2 repeat-Rs1544689-D2S123-cen (table 4). The 1906C-bearing haplotype in individual JHU SG (family 7) (tables 1 and 4) is tel-4-3-*A-2-A-3-G-[288-255-177-A-G-C]-139-143-250-C-6-cen (the alleles are given in the same order as are the loci, the intragenic markers are indicated by square brackets, the mutation is in boldface, and the asterisk indicates that this locus has no linkage information in this individual; details are shown in table 4).

The genotypes from representative mutation carriers are shown in table 4. Markers from the distal flanking marker D2S2306 to the proximal marker CA-2 were shared by 9 of 15 probands for whom we had data on all markers; this distance is ~10.3 Mb (fig. 4). In individual JHU SG, in whom we were able to study each chromosome separately, the mutation occurs on a haplotype where the allele at D2S2306 is 3—rather than 4, which appears to be linked in all other families tested. If the linked haplotype truly does break down somewhere between Rs896213 and D2S2306 but extends to CA-2 on the centromeric side of *MSH2*, then the linked region is 3.2 Mb in length; this region is shared by 12 of 15 probands. A breakdown distal to Rs896213 is likely, because 2 of 13 tested individuals did not share the common haplotype at SNP marker Rs868542, which is only 167 kb telomeric of Rs896213. In a region closer to the gene, two individuals (S-M112 and 8080894) (table 4) do not carry the linked allele (i.e., allele 2) at D2S391. Because this is a microsatellite marker, it is possible that this represents a marker mutation (these individuals are 3,4 and 3,3, respectively, at this locus). More conservatively, if one considers that the haplotype breaks down here but extends from Rs1374749 proximally to CA-2, then the linked region is 2.03 Mb in length (seen in 14 of 15 probands; fig. 4). It can be seen in table 4 that alleles for the centromeric markers CA-3 and CA-2 are different in MON702 compared with all other mutation carriers, so, conservatively, the linked haplotype ends <95 kb 3' of *MSH2*. Therefore, the eight-marker haplotype from Rs1374749 to the mutation itself (A-3-G-288-255-177-A-G) is shared by all 14 of the families in which all the markers were tested. In this case, the minimum linked region in this study is ~1.91 Mb long (figs. 3 and 4). Because, in two families, Rs1374749 could not be tested in probands, all 16 probands share a slightly smaller interval, ~1.33 Mb (fig. 4). We checked the allele frequencies of 15 of the markers used in this study, to establish whether the linked alleles were common in the Jewish population. In 48–70 chromosomes from unaffected Ashkenazi Jewish individuals, the allele frequencies for the linked markers telomeric to the gene (fig. 3) were as follows: D2S391, .193; Rs1374749, .52; D2S2227, .276; and Rs919883, .397.

Only at Rs1374749 was the linked allele the most commonly observed allele in the control individuals studied. Statistical tests show that, for extragenic markers D2S2306, Rs896213, D2S391, Rs919883, CA-3, CA-1, and CA-2, the linked allele is statistically significantly more frequent in mutation carriers than in control individuals ($P = .0001-.04$; data not shown). In summary, the shortest linked region, seen in all 16 probands tested, is 1.33 Mb, whereas the longest possible region of sharing is ~10.3 Mb, but both microsatellite and SNP results make this degree of sharing unlikely (table 4).

We used the PHASE program to estimate the frequency of the haplotype bearing the *MSH2**1906G→C mutation in the Ashkenazi Jewish population. The statistical basis of this new method is discussed briefly in the Subjects, Material, and Methods section. We genotyped 54 randomly selected unaffected individuals, at six intragenic markers, as well as at three 3' flanking markers—CA-1, CA-2, and CA-3 (table 4 and fig. 3). By seeding the program with (a) the identified linked intragenic haplotype and (b) 11 other phased unlinked haplotypes from individuals whose genotypes are shown in table 4, we were able to predict with 90% probability that four to six chromosomes (depending on the simulation) in the 54 individuals carry the disease-linked intragenic haplotype. None of these chromosomes carries the *MSH2**1906G→C mutation. This suggests that the intragenic portion of the linked haplotype is present in ~10% of unaffected Ashkenazi Jewish individuals but is not associated with the disease-causing mutation. However, no control chromosomes were predicted to match the disease-associated haplotype when markers CA-1, CA-2, and CA-3 were included in the analysis.

Discussion

In the present article, we have described the identification and characterization of a founder mutation in *MSH2*. This base-pair substitution, 1906G→C, results in the alteration of the amino acid sequence from that of alanine to that of proline. On the basis of segregation, MSI analyses, and a yeast assay (Andreutti-Zaugg et al. 1997) in a single Ashkenazi Jewish family, we originally predicted that this mutation would be disease causing, but we did not have sufficient data to be completely convinced of this (Yuan et al. 1999). The present study, together with recent data reporting that the addition of a single human chromosome containing the *MSH2**1906G→C mutation did not correct mismatch-repair deficiency in *Msh2*^{-/-} mouse cells (Marra et al. 2001), confirms that this variant is a bona fide disease-causing mutation. Importantly, the immunohistochemical data presented here show that the protein is unstable. The presence of this mutation in probands from 16 unrelated families (in which a total of 25 Ashkenazi

Jewish individuals were tested) who all share the same intragenic haplotype identify *MSH2**1906G→C as the first founder mutation in *MSH2* in the Jewish population. This mutation can be added to the list of founder mutations that have been identified in Jews (Ostrer 2001).

Our previous report provided a clue that this mutation might not be frequent in those with colorectal cancer, because we failed to identify this mutation in 196 Ashkenazi Jews with colorectal cancer. However, the mean age at diagnosis in this series was 71.7 years (range 39.8–92.1 years), and the age at diagnosis in 23 of these individuals was <60 years (M. Redston, personal communication); thus, few germline mutations would be expected in this series. Only 15 of the 196 tumors showed MSI-H (Yuan et al. 1999), and, because 5%–15% of MSI-H colorectal cancer is due to germline mutations in *MSH2*, in retrospect we now know that our original study had insufficient power to detect this founder mutation in *MSH2*.

We studied several series of unselected Ashkenazi Jews with or without cancer, allowing us to estimate the frequency of the *MSH2**1906G→C mutation in these groups. The results for those affected with cancer are shown in table 5. Particularly noteworthy are the findings in the three series of colorectal cancers—686 from northern Israel, 355 from Tel Aviv, and 108 from MSKCC in New York. Three mutation carriers (diagnosed at ages 45, 52, and 75 years) were identified in the northern-Israeli series, four (diagnosed at ages 36, 52, 60, and 69 years) in the Tel Aviv series, and one (diagnosed at age 28 years) in the MSKCC series. Although, clearly, the northern-Israeli and New York cases and control individuals are not completely comparable, it may be instructive to compare the frequency of the mutation in a large series of Jewish cases and control individuals. Thus, eight mutation carriers were identified among these 1,149 cases from northern Israel and New York, and none were found among 1,588 control individuals from the same two populations ($P = .00095$). In our previous report, we identified no carriers among 196 Ashkenazi Jewish individuals with colorectal cancer who were from Toronto. If we combine all the results obtained in Ashkenazi Jews with colorectal cancer, 8/1,345 (0.59%; 95% CI 0.26%–1.17%) affected individuals carry this mutation. We do not have the precise ages at diagnosis for the Tel Aviv series, but, when the data from patients diagnosed at age <60 years in the Toronto, MSKCC, and northern-Israel series are combined, 3/140 (2.1%; 95% CI 0.44%–6.1%) individuals with colorectal cancer diagnosed at age <60 years carried this mutation (table 5). These results suggest that the *MSH2**1906G→C mutation cannot account for a large proportion of colorectal cancer; however, a significant fraction (10%–65%) of Amsterdam

criteria-fulfilling HNPCC occurring in the Ashkenazi Jewish population is due to this single missense mutation.

Family-based studies are, by their nature, biased toward kindreds with numerous cases of cancer, but it is nevertheless notable that the range of cancers seen in mutation-bearing families is wide (table 1 and fig. 1) and is in keeping with previous data that have suggested that *MSH2* mutations result in a cancer phenotype broader than that resulting from *MLH1* mutations (Vasen et al. 2001). Taken together, the spectrum of cancers observed in carriers of the *MSH2**1906G→C mutation imply that vigilance will be required when such individuals are followed and that screening for cancer at all potential sites will be difficult. The presence of urothelial cancers in more than one member of several kindreds (table 1) is particularly noteworthy.

In all 16 families genotyped at markers flanking *MSH2*, there is a clear and complete breakdown of the linked haplotype at D2S2331 (telomeric) and at D2S123 (centromeric), resulting in a maximum shared region that is ~15.7 Mb; 14 families share a region ≤1.91 Mb (from Rs137479 to the mutation itself). However, recent physical- and recombination-map data (Kong et al. 2002) suggest that it is possible that Rs137479 is telomeric—not centromeric—to Rs896213, as shown in figure 3. The precise position of D2S391 is also uncertain (fig. 3). If the order is as described in the genetic map presented by Kong et al. (2002), then it would slightly alter the length of the conserved haplotype. However, we believe that the most parsimonious interpretation of our data favors the map order indicated in table 4 and figure 3.

It is interesting to note that, using the PHASE program, we can predict that the intragenic haplotype will be observed in ~10% of Ashkenazi Jewish individuals but that the program predicts that there would be no unaffected individuals who share the haplotype once we extend it beyond the boundaries of the gene. If we consider haplotype, genotype, PHASE, and mutation-frequency data, it is reasonable to conclude that the mutation owes its origin to a founder who lived 200–500 years ago. Consistent with these observations, the size of the shared haplotype may extend as far as 10 Mb, historical recombination events having not yet broken the haplotypes into smaller segments. Moreover, if the reason why other cancer-related founder mutations in the Ashkenazi Jewish population, such as *BRCA1**187delAG are common (up to 1% of Ashkenazi Jewish individuals carry this mutation), is genetic drift, then, clearly, mutation frequency can drift up or down. Therefore, given the size of the Ashkenazi Jewish population worldwide, the relative rarity of this mutation may be a combination of recent origin and chance.

The exon 5 *MSH2* mutation is a founder mutation within Newfoundland, but it has several separate origins worldwide (Desai et al. 2000). Only three other founders in mismatch-repair genes have been described previously; all are in *MLH1*. de la Chapelle and colleagues described two different founder mutations in *MLH1*, whose origins were placed at ~400–1,075 years ago (mutation 1) and at only 125–525 years ago (mutation 2) (Moisio et al. 1996). In a study of 535 Finnish individuals with incident colorectal cancer, 18 germline *MLH1* and *MSH2* mutations were identified. Among these 18 individuals, 13 carried a founder mutation (9 had mutation 1, and 4 had mutation 2). Thus, just testing for these two founder mutations would detect 72% of all mismatch-repair-gene mutations detected in this series, and these two mutations account for 2.4% (95% CI 1.3%–4.1%) of all colorectal cancer occurring in the southeastern part of Finland (Salovaara et al. 2000). These two mutations probably have a prevalence higher than that of the *MSH2**1906G→C mutation in the Ashkenazi Jewish population. The age of the third founder *MLH1* mutation could not be determined accurately, because of the small number of available chromosomes (Hutter et al. 1996), although more-recent investigations have suggested that this mutation is ≥400 years old (P. Hutter, personal communication).

In the Ashkenazi Jewish population, several other founder mutations have been identified in cancer-related genes such as *BLM*, *BRCA1*, *BRCA2*, *FANCC*, and *APC*. The heterozygote frequency of these alleles varies from 1/16 for I1307K in *APC* to 1/107 for the 2281:del6ins7 mutation in *BLM* (Ostrer 2001). The population frequency of the *MSH2**1906G→C mutation has not been accurately determined in a single series. When we combine the data presented here with those from our previous study, in which we typed 100 control individuals, none of 1,688 unaffected Ashkenazi Jewish individuals carry this mutation (upper 95% CI 0.22%, or 1/458), suggesting that, in this population, it is rarer than previously reported cancer-causing alleles. Larger population-based studies will be required to more precisely estimate the population frequency of this allele.

In the present article, we have described the identification and characterization of a previously unrecognized founder mutation in *MSH2*. This mutation, at nucleotide 1906, codon 636, results in the substitution of a proline for an alanine. Immunohistochemical analyses of tumors that carry the A636P mutation show that the mutant protein is unstable. Molecular modeling suggests that this change results in steric hindrance and, possibly, interference with ATP hydrolysis. The mutation has been identified in 25 apparently unrelated families, most of which are known to be of Ashkenazi Jewish origin. By screening for this mutation in several unselected Ashkenazi Jewish populations, it has been

determined that the *MSH2**1906G→C mutation is a rare cause of colorectal cancer in this population but that it probably accounts for ≥10% of all Amsterdam criteria-fulfilling HNPCC in the Ashkenazi Jewish population. Because of this, it may be prudent, if Ashkenazi Jewish ancestry is documented or suspected, to assay for this mutation before proceeding to complete molecular analysis of *MSH2* in Amsterdam criteria-fulfilling kindreds in which a mismatch-repair-gene mutation is suspected. This will be particularly useful if immunohistochemistry documents a loss of *MSH2* protein expression in colorectal cancer.

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Electronic-Database Information

Accession numbers and URLs for data presented herein are as follows:

Genome Database, The, <http://gdbwww.gdb.org>
 International Collaborative Group on Hereditary Non-Polyposis Colorectal Cancer ("Choose a Mutation Database" Web page), <http://www.nfdht.nl/database/mdbchoice.htm> (for map information and mutations in mismatch-repair genes)
 National Center for Biotechnology Information "Single Nucleotide Polymorphism" Web page, <http://www.ncbi.nlm.nih.gov/SNP/>
 National Laboratory for the Genetics of Israeli Populations (Tel Aviv University), <http://www.tau.ac.il/medicine/NLGP/catalog.htm>
 Online Mendelian Inheritance in Man (OMIM), <http://www.ncbi.nlm.nih.gov/Omim/> (for *MSH2* [MIM 120435], *MSH1* [MIM 120436], and *HNPCC* [MIM 114500])
 SNP Consortium Ltd., The, <http://snp.cshl.org/index.html>
 University of California, Santa Cruz, "BLAST Search Genome" Web page, <http://genome.ucsc.edu/cgi-bin/hgBlat?command=start>
 University of California, Santa Cruz, "UCSC Genome Informatics" ("Golden Path") Web page, <http://genome.ucsc.edu/goldenPath/mapPlots/>

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